Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** **SERIAL NUMBER:** 09/348,354

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

AUG 2 1 2000

TECH CENTER 1600/2900

1 ____	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2 ____	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3 ____	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4 ____	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5 ____	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6 ____	Variable Length	Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
7 ____	PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
8 ____	Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: **(2) INFORMATION FOR SEQ ID NO:X:** **(i) SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS") **(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:** **This sequence is intentionally skipped** Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9 ✓	Skipped Sequences (NEW RULES)	Sequence(s) #80 missing. If intentional, please use the following format for each skipped sequence. **<210> sequence id number** **<400> sequence id number** **000**
10 ✓	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
11 ____	Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.
12 ____	Use of <220>Feature (NEW RULES)	Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" **Please explain source of genetic material in <220> to <223> section.** (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
13 ____	PatentIn ver. 2.0 "bug"	**Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

Does Not Comply
Corrected Diskette Needed

1633

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/348,354

DATE: 08/15/2000
TIME: 15:21:47

Input Set : A:\PTO.txt
Output Set: N:\CRF3\08152000\I348354.raw

See pp. 1, 4, 5

3 <110> APPLICANT: Havenga, Menzo
5 <120> TITLE OF INVENTION: Chimeric Adenoviruses
7 <130> FILE REFERENCE: 2183-4123us
9 <140> CURRENT APPLICATION NUMBER: 09/348,354
10 <141> CURRENT FILING DATE: 1999-07-07
E--> 12 <160> NUMBER OF SEQ ID NOS: 85
14 <170> SOFTWARE: PatentIn Ver. 2.1

Sequence #80 missing, causing miscount of sequences.
85 input, 84 counted.

ERRORED SEQUENCES

3394 <210> SEQ ID NO: 79
3395 <211> LENGTH: 21 -> 35
3396 <212> TYPE: DNA
3397 <213> ORGANISM: Primer/Oligonucleotide
3399 <400> SEQUENCE: 79
E--> 3400 gctcgatgta caatgaggcg tgcggtggtg tcttc
E--> 3403 <210> SEQ ID NO: 81

14 -> 35

Error in base count

VERIFICATION SUMMARY DATE: 08/15/2000
PATENT APPLICATION: US/09/348,354 TIME: 15:21:48

Input Set : A:\PTO.txt
Output Set: N:\CRF3\08152000\I348354.raw

L:298 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:298 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:298 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:298 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
L:298 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
L:301 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:301 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:301 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:301 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
M:340 Repeated in SeqNo=16
L:304 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:304 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:304 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:304 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
L:307 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:307 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:307 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:307 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
L:370 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:370 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:370 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:370 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
L:696 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:21
L:696 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:696 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:696 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:696 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:21
L:976 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25
L:976 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:976 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:976 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:976 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25
L:979 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25
L:979 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:979 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:979 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
M:340 Repeated in SeqNo=25
L:982 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25
L:982 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:982 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:982 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:991 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25
L:991 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:991 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:991 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1000 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25
L:1000 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1000 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25

VERIFICATION SUMMARY DATE: 08/15/2000
PATENT APPLICATION: US/09/348,354 TIME: 15:21:48

Input Set : A:\PTO.txt
Output Set: N:\CRF3\08152000\I348354.raw

L:1000 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1006 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25
L:1006 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1006 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1006 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1532 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:32
L:1532 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
L:1532 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
M:340 Repeated in SeqNo=32
L:1723 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
L:1760 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:35
M:340 Repeated in SeqNo=35
L:2252 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:41
L:3400 M:254 E: No. of Bases conflict, LENGTH:Input:14 Counted:35 SEQ:79
L:3400 M:252 E: No. of Seq. differs, <211>LENGTH:Input:21 Found:35 SEQ:79
L:3403 M:214 E: (33) Seq.# missing, SEQ ID NO:80
L:12 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (85) Counted (84)

<210> 79
<211> 21
<212> DNA
<213> Primer/Oligonucleotide

<400> 79
gctcgatgta caatgaggcg tgcggtggtg tcttc
14

→ Sequence # 80? If skipped intentionally, please use correct format as shown in #9 on Error Summary Sheet.

<210> 81
<211> 34
<212> DNA
<213> Primer/Oligonucleotide

<400> 81
gctcgactta agttagaagg tgcgactgga aagc

p. 5 . . .

09/348,354

As per new sequence rules, all "n's" or "Xaa's" in sequences must have <220> to <223> features. See #10 on Error Summary Sheet.

Please check entire sequence listing as this same error has been indicated throughout.

<210> 16
<211> 391
<212> PRT
<213> Human Adenovirus 13 Fiber Protein

<400> 16
Xaa Xaa Xaa Xaa Xaa Ser Ala Pro Thr Ile Phe Met Leu Leu Gln Met
1 5 10 15

Lys Arg Ala Arg Ser Ser Xaa Asp Thr Phe Asn Pro Val Tyr Pro Tyr
20 25 30

Gly Tyr Ala Arg Asn Gln Asn Ile Xaa Phe Xaa Thr Pro Pro Phe Val
35 40 45

Xaa Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu Lys
50 55 60

Leu Ala Asp Pro Ile Thr Ile Ala Asn Gly Asp Val Ser Leu Lys Val
65 70 75 80

Gly Gly Gly Leu Thr Leu Gln Glu Gly Ser Leu Thr Val Asp Pro Lys
85 90 95

Ala Pro Leu Gln Leu Ala Asn Asp Lys Lys Leu Glu Leu Val Tyr Asp
100 105 110

Asp Pro Phe Glu Val Ser Thr Asn Lys Leu Ser Leu Lys Val Gly His
115 120 125

Gly Leu Lys Val Leu Asp Asp Lys Ser Ala Gly Gly Leu Lys Asp Leu
130 135 140

Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Ile Glu Asn
145 150 155 160

Leu Gln Asn Asp Asp Gly Ser Ser Arg Gly Val Gly Ile Asn Val Arg
165 170 175

Leu Gly Thr Asp Gly Gly Leu Ser Phe Asp Arg Lys Gly Glu Leu Val
180 185 190

Ala Trp Asn Arg Lys Asp Asp Arg Arg Thr Leu Trp Thr Thr Pro Asp
195 200 205

Pro Ser Pro Asn Cys Lys Ala Glu Thr Glu Lys Asp Ser Lys Leu Thr
210 215 220

Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Ile
225 230 235 240

Ile Val Leu Lys Gly Lys Tyr Glu Phe Val Lys Lys Glu Thr Glu Pro
245 250 255

Lys Ser Phe Asp Val Lys Leu Leu Phe Asp Ser Lys Gly Val Leu Leu
260 265 270

The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.